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c) identifying one or more heterologous oligonucleotide sequences that are similar to one or more of the mutually overlapping oligonucleotide sequence fragments, wherein the one or more heterologous oligonucleotide sequences thus identified are from a different species than the target nucleic acid sequence.

11. (New) The process of claim 10, wherein said identifying of one or more heterologous oligonucleotide sequences further comprises isolating one or more of the heterologous oligonucleotide sequences thus identified.

12. (New) The process of claim 10, wherein the one or more heterologous oligonucleotide sequences are selected from SEQ ID NOS. 1, 2, 3, 4, 5, 6, 7, 8 and 9.

13. (New) The process of claim 10, wherein the mutually overlapping oligonucleotide sequence fragments each comprise from about 1 to about 100 bases.

14. (New) The process of claim 13, wherein the mutually overlapping oligonucleotide sequence fragments each comprise from about 25 to about 75 bases.

15. (New) The process of claim 14, wherein the mutually overlapping oligonucleotide sequence fragments each comprise from about 30 to about 50 bases.

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16. (New) The process of claim 15, wherein the mutually overlapping oligonucleotide sequence fragments are generated by fragmenting a conserved region of a virus genome.

17. (New) The process of claim 16, wherein the virus genome is from a Hepatitis C Virus (HCV).

18. (New) The process of claim 10, wherein the one or more heterologous oligonucleotide sequences are identified from a gene library.

19. (New) The process of claim 10, wherein the one or more heterologous oligonucleotide sequences are identified in a DNA sequence database.

20. (New) The process of claim 10, wherein said identifying of one or more heterologous oligonucleotide sequences further comprises: (i) identifying basepair mismatches between one or more of the heterologous oligonucleotide sequences and one or more of the mutually overlapping oligonucleotide sequence fragments, and (ii) replacing any mismatched base pairs thus identified in the one or more heterologous oligonucleotide sequences with a universal base.

21. (New) The process of claim 20, wherein the universal base is inosine.

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28. (New) The reagent set of claim 26, wherein one of the primers is labeled

29. (New) The reagent set of claim 28, wherein the labeled primer does not

30. (New) A reagent set for use in identifying a target nucleic acid sequence

31. (New) The reagent set of claim 30, wherein the oligonucleotide probe is

32. (New) The reagent set of claim 30, wherein the oligonucleotide probe

33. (New) The reagent set of claim 32, wherein the fluorescent dyes comprise

34. (New) The reagent set of claim 32, wherein the fluorescent dyes are

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